

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Yu, Guo-Liang
Ni, Jian
Dixit, Vishva
Gentz, Reiner L.
Dillon, Patrick J.
- (ii) TITLE OF INVENTION: Death Domain Containing Receptors
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 - (B) STREET: 1100 New York Ave., NW, Suite 600
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: HERewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: Not Yet Assigned
 - (B) FILING DATE: 06-FEB-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/028,711
 - (B) FILING DATE: 17-OCT-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/013,285
 - (B) FILING DATE: 12-MAR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Steffe, Eric K.
 - (B) REGISTRATION NUMBER: 36,688
 - (C) REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-371-2600
 - (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 198..1481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CATGGGTGGG GGTGGGGGCG CTGCTGGATT CCTGCTCTGG TGGAGGGGAA ACTTGTGAGG	60
GGCTGGTAAG CGCCCCCTCC GAAGCCTGGT GTGTGCGCGG GGGGAAGGAA GTTAGTTTCC	120
TCTCCACCCA TGGGCACCCC TTCTGCCCGG GGCCTGGGAA GTGGGCTGCT CTGTGGGCAA	180
ATGCTGGGGC CTCTGAA ATG GAG GAG ACG CAG CAG GGA GAG GCC CCA CGT	230
Met Glu Glu Thr Gln Gln Gly Glu Ala Pro Arg	
1 5 10	
GGG CAG CTG CGC GGA GAG TCA GCA GCA CCT GTC CCC CAG GCG CTC CTC	278
Gly Gln Leu Arg Gly Glu Ser Ala Ala Pro Val Pro Gln Ala Leu Leu	
15 20 25	
CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT CGT AGC CCC AGG	326
Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg	
30 35 40	
TGT GAC TGT GCC GGT GAC TTC CAC AAG AAG ATT GGT CTG TTT TGT TGC	374
Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys	
45 50 55	
AGA GGC TGC CCA GCG GGG CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC	422
Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro	
60 65 70 75	
TGC GGC AAC TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC	470
Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala	
80 85 90	
TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG GCC TGT GAT	518
Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp	
95 100 105	
GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC TGT TCA GCA GTG GCC GAC	566
Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp	
110 115 120	

ACC CGC TGT GGC TGT AAG CCA GGC TGG TTT GTG GAG TGC CAG GTC AGC	614
Thr Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser	
125 130 135	
CAA TGT GTC AGC AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC	662
Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys	
140 145 150 155	
GGG GCC CTG CAC CGC CAC ACA CGG CTA CTC TGT TCC CGC AGA GAT ACT	710
Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr	
160 165 170	
GAC TGT GGG ACC TGC CTG CCT GGC TTC TAT GAA CAT GGC GAT GGC TGC	758
Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys	
175 180 185	
GTG TCC TGC CCC ACG AGC ACC CTG GGG AGC TGT CCA GAG CGC TGT GCC	806
Val Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala	
190 195 200	
GCT GTC TGT GGC TGG AGG CAG ATG TTC TGG GTC CAG GTG CTC CTG GCT	854
Ala Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala	
205 210 215	
GGC CTT GTG GTC CCC CTC CTG CTT GGG GCC ACC CTG ACC TAC ACA TAC	902
Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr	
220 225 230 235	
CGC CAC TGC TGG CCT CAC AAG CCC CTG GTT ACT GCA GAT GAA GCT GGG	950
Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly	
240 245 250	
ATG GAG GCT CTG ACC CCA CCA CCG GCC ACC CAT CTG TCA CCC TTG GAC	998
Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp	
255 260 265	
AGC GCC CAC ACC CTT CTA GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC	1046
Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys	
270 275 280	
ACC GTC CAG TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC	1094
Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr	
285 290 295	
CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC CAG TTG CCC	1142
Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro	
300 305 310 315	
AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC ACA CTC TCG CCA GAG TCC	1190
Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser	
320 325 330	
CCA GCC GGC TCG CCA GCC ATG ATG CTG CAG CCG GGC CCG CAG CTC TAC	1238
Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr	
335 340 345	

GAC GTG ATG GAC GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC	1286
Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg	
350 355 360	
ACG CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG GAG ATC	1334
Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile	
365 370 375	
GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC AAG CGC TGG CGC CAG	1382
Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln	
380 385 390 395	
CAG CAG CCC GCG GGC CTC GGA GCC GTT TAC GCG GCC CTG GAG CGC ATG	1430
Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met	
400 405 410	
GGG CTG GAC GGC TGC GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC	1478
Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly	
415 420 425	
CCG TGACACGGCG CCCACTTGCC ACCTAGGCGC TCTGGTGGCC CTTGCAGAAG	1531
Pro	
CCCTAAGTAC GGTTACTTAT GCGTGTAGAC ATTTTATGTC ACTTATTAAG CCGCTGGCAC	1591
GGCCCTGCGT AGCAGCACCA GCCGGCCCCA CCCCTGCTCG CCCCTATCGC TCCAGCCAAG	1651
GCGAAGAAGC ACGAACGAAT GTCGAGAGGG GGTGAAGACA TTTCTCAACT TCTCGGCCGG	1711
AGTTTGGCTG AGATCGCGGT ATTAAATCTG TGAAAGAAAA CAAAACAAAA CAAAAAAAAA	1771
AAAAAAAAAA AA	1783

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 428 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Glu	Thr	Gln	Gln	Gly	Glu	Ala	Pro	Arg	Gly	Gln	Leu	Arg	Gly
1				5					10					15	
Glu	Ser	Ala	Ala	Pro	Val	Pro	Gln	Ala	Leu	Leu	Leu	Val	Leu	Leu	Gly
			20					25					30		
Ala	Arg	Ala	Gln	Gly	Gly	Thr	Arg	Ser	Pro	Arg	Cys	Asp	Cys	Ala	Gly
			35				40					45			

Asp	Phe	His	Lys	Lys	Ile	Gly	Leu	Phe	Cys	Cys	Arg	Gly	Cys	Pro	Ala	50	55	60
Gly	His	Tyr	Leu	Lys	Ala	Pro	Cys	Thr	Glu	Pro	Cys	Gly	Asn	Ser	Thr	65	70	75
Cys	Leu	Val	Cys	Pro	Gln	Asp	Thr	Phe	Leu	Ala	Trp	Glu	Asn	His	His	85	90	95
Asn	Ser	Glu	Cys	Ala	Arg	Cys	Gln	Ala	Cys	Asp	Glu	Gln	Ala	Ser	Gln	100	105	110
Val	Ala	Leu	Glu	Asn	Cys	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys	Gly	Cys	115	120	125
Lys	Pro	Gly	Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	Gln	Cys	Val	Ser	Ser	130	135	140
Ser	Pro	Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	Gly	Ala	Leu	His	Arg	145	150	155
His	Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	Asp	Cys	Gly	Thr	Cys	165	170	175
Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro	Thr	180	185	190
Ser	Thr	Leu	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	Ala	Val	Cys	Gly	Trp	195	200	205
Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	Gly	Leu	Val	Val	Pro	210	215	220
Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	Tyr	Arg	His	Cys	Trp	Pro	225	230	235
His	Lys	Pro	Leu	Val	Thr	Ala	Asp	Glu	Ala	Gly	Met	Glu	Ala	Leu	Thr	245	250	255
Pro	Pro	Pro	Ala	Thr	His	Leu	Ser	Pro	Leu	Asp	Ser	Ala	His	Thr	Leu	260	265	270
Leu	Ala	Pro	Pro	Asp	Ser	Ser	Glu	Lys	Ile	Cys	Thr	Val	Gln	Leu	Val	275	280	285
Gly	Asn	Ser	Trp	Thr	Pro	Gly	Tyr	Pro	Glu	Thr	Gln	Glu	Ala	Leu	Cys	290	295	300
Pro	Gln	Val	Thr	Trp	Ser	Trp	Asp	Gln	Leu	Pro	Ser	Arg	Ala	Leu	Gly	305	310	315
Pro	Ala	Ala	Ala	Pro	Thr	Leu	Ser	Pro	Glu	Ser	Pro	Ala	Gly	Ser	Pro	325	330	335
Ala	Met	Met	Leu	Gln	Pro	Gly	Pro	Gln	Leu	Tyr	Asp	Val	Met	Asp	Ala			

340	345	350
Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg		
355	360	365
Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile Gly Arg Phe Arg Asp		
370	375	380
Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly		
385	390	395
Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys		
405	410	415
Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro		
420	425	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GAG CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC CTC	48
Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu	
430	435
CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT CGT AGC CCC AGG	96
Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg	
445	450
TGT GAC TGT GCC GGT GAC TTC CAC AAG AAG ATT GGT CTG TTT TGT TGC	144
Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys	
465	470
AGA GGC TGC CCA GCG GGG CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC	192
Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro	
480	485
TGC GGC AAC TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC	240
Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala	
495	500
	505

TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG GCC TGT GAT	288
Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp	
510 515 520	
GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC TGT TCA GCA GTG GCC GAC	336
Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp	
525 530 535 540	
ACC CGC TGT GGC TGT AAG CCA GGC TGG TTT GTG GAG TGC CAG GTC AGC	384
Thr Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser	
545 550 555	
CAA TGT GTC AGC AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC	432
Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys	
560 565 570	
GGG GCC CTG CAC CGC CAC ACA CGG CTA CTC TGT TCC CGC AGA GAT ACT	480
Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr	
575 580 585	
GAC TGT GGG ACC TGC CTG CCT GGC TTC TAT GAA CAT GGC GAT GGC TGC	528
Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys	
590 595 600	
GTG TCC TGC CCC ACG AGC ACC CTG GGG AGC TGT CCA GAG CGC TGT GCC	576
Val Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala	
605 610 615 620	
GCT GTC TGT GGC TGG AGG CAG ATG TTC TGG GTC CAG GTG CTC CTG GCT	624
Ala Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala	
625 630 635	
GGC CTT GTG GTC CCC CTC CTG CTT GGG GCC ACC CTG ACC TAC ACA TAC	672
Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr	
640 645 650	
CGC CAC TGC TGG CCT CAC AAG CCC CTG GTT ACT GCA GAT GAA GCT GGG	720
Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly	
655 660 665	
ATG GAG GCT CTG ACC CCA CCA CCG GCC ACC CAT CTG TCA CCC TTG GAC	768
Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp	
670 675 680	
AGC GCC CAC ACC CTT CTA GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC	816
Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys	
685 690 695 700	
ACC GTC CAG TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC	864
Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr	
705 710 715	
CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC CAG TTG CCC	912
Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro	
720 725 730	

AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC ACA CTC TCG CCA GAG TCC	960
Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser	
735 740 745	
CCA GCC GGC TCG CCA GCC ATG ATG CTG CAG CCG GGC CCG CAG CTC TAC	1008
Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr	
750 755 760	
GAC GTG ATG GAC GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC	1056
Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg	
765 770 775 780	
ACG CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG GAG ATC	1104
Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile	
785 790 795	
GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC AAG CGC TGG CGC CAG	1152
Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln	
800 805 810	
CAG CAG CCC GCG GGC CTC GGA GCC GTT TAC GCG GCC CTG GAG CGC ATG	1200
Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met	
815 820 825	
GGG CTG GAC GGC TGC GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC	1248
Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly	
830 835 840	
CCG TGA	1254
Pro	
845	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu Leu	
1 5 10 15	
Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg	
20 25 30	
Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu Phe Cys Cys	
35 40 45	
Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro Cys Thr Glu Pro	
50 55 60	

Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
 65 70 75 80
 Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln Ala Cys Asp
 85 90 95
 Glu Gln Ala Ser Gln Val Ala Leu Glu Asn Cys Ser Ala Val Ala Asp
 100 105 110
 Thr Arg Cys Gly Cys Lys Pro Gly Trp Phe Val Glu Cys Gln Val Ser
 115 120 125
 Gln Cys Val Ser Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys
 130 135 140
 Gly Ala Leu His Arg His Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr
 145 150 155 160
 Asp Cys Gly Thr Cys Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys
 165 170 175
 Val Ser Cys Pro Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala
 180 185 190
 Ala Val Cys Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala
 195 200 205
 Gly Leu Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr
 210 215 220
 Arg His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly
 225 230 235 240
 Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu Asp
 245 250 255
 Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys
 260 265 270
 Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr
 275 280 285
 Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp Gln Leu Pro
 290 295 300
 Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser
 305 310 315 320
 Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr
 325 330 335
 Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg
 340 345 350
 Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile

355		360		365
Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln				
370		375		380
Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met				
385		390		395 400
Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly				
	405		410	415
Pro				

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu		
1	5	10 15
Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro		
	20	25 30
His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys		
	35	40 45
Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys		
	50	55 60
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp		
65	70	75 80
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu		
	85	90 95
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val		
	100	105 110
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg		
	115	120 125
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe		
	130	135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu			
145	150	155	160
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu			
	165	170	175
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr			
	180	185	190
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser			
	195	200	205
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu			
	210	215	220
Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys			
225	230	235	240
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu			
	245	250	255
Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser			
	260	265	270
Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val			
	275	280	285
Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys			
	290	295	300
Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly			
305	310	315	320
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn			
	325	330	335
Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp			
	340	345	350
Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro			
	355	360	365
Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu			
	370	375	380
Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln			
385	390	395	400
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala			
	405	410	415
Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly			
	420	425	430
Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro			

435

440

445

Pro Ala Pro Ser Leu Leu Arg
450 455

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
1 5 10 15

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
20 25 30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
35 40 45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
50 55 60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
65 70 75 80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
85 90 95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
100 105 110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
115 120 125

Cys Lys Pro Asn Phe Phe Gln Asn Ser Thr Val Cys Glu His Cys Asp
130 135 140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
145 150 155 160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
165 170 175

Leu Cys Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
180 185 190

Lys	Glu	Val	Gln	Lys	Thr	Cys	Arg	Lys	His	Arg	Lys	Glu	Asn	Gln	Gly
	195						200					205			
Ser	His	Glu	Ser	Pro	Thr	Leu	Asn	Pro	Glu	Thr	Val	Ala	Ile	Asn	Leu
	210					215					220				
Ser	Asp	Val	Asp	Leu	Ser	Lys	Tyr	Ile	Thr	Thr	Ile	Ala	Gly	Val	Met
225					230				235					240	
Thr	Leu	Ser	Gln	Val	Lys	Gly	Phe	Val	Arg	Lys	Asn	Gly	Val	Asn	Glu
			245						250					255	
Ala	Lys	Ile	Asp	Glu	Ile	Lys	Asn	Asp	Asn	Val	Gln	Asp	Thr	Ala	Glu
			260					265					270		
Gln	Lys	Val	Gln	Leu	Leu	Arg	Asn	Trp	His	Gln	Leu	His	Gly	Lys	Lys
	275						280					285			
Glu	Ala	Tyr	Asp	Thr	Leu	Ile	Lys	Asp	Leu	Lys	Lys	Ala	Asn	Leu	Cys
	290					295					300				
Thr	Leu	Ala	Glu	Lys	Ile	Gln	Thr	Ile	Ile	Leu	Lys	Asp	Ile	Thr	Ser
305					310					315				320	
Asp	Ser	Glu	Asn	Ser	Asn	Phe	Arg	Asn	Glu	Ile	Gln	Ser	Leu	Val	
			325					330					335		

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCCATGGG GGCCCGGCGG CAG

23

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGAAGCTTC TAGGACCCAG AACATCTGCC

30

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCGGATCCG CCATCATGGA GGAGACGCAG CAG

33

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGATCCG CCATCATGGA GCAGCGGCCG CGG

33

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGTCTAGAT CAAAGCGTAG TCTGGGACGT CGTATGGGTA CGGGCCGCGC TGCA

54

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGGATCCG CCATCATGGA GGAGACGCAG CAG

33

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGCGGATCCG CCATCATGGA GCAGCGGCCG CGG

33

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCGGATCCT CACGGGCCGC GCTGCA

26

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCGGATCCG CCATCATGGA GGAGACGCAG CAG

33

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCGGATCCG CCATCATGGA GCAGCGGCCG CGG

33

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCGAGATCTA GTCTGGACCC AGAACATCTG CCTCC

35